

SEQUENCE LISTING

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ANALYSIS OF ANTI-SENSE MODULATION OF PI3K p85 EXPRESSION

<210> 1  
<211> 1372  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 43) ... (2217)

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 Met Ser Ala Glu  
 1  
 ggg tac cag tac aga gcg ctg tat gat tat aaa aag gaa aga gaa gaa 102  
 Gly Tyr Gln Tyr Arg Ala Leu Tyr Asp Tyr Lys Lys Glu Arg Glu Glu  
 5 10 15 20  
 gat att gac ttg cac ttg ggt gac ata ttg act gtg aat aaa ggg tcc 150  
 Asp Ile Asp Leu His Leu Gly Asp Ile Leu Thr Val Asn Lys Gly Ser  
 25 30 35  
 tta gta gct ctt gga ttc agt gat gga cag gaa gcc agg cct gaa gaa 198  
 Leu Val Ala Leu Gly Phe Ser Asp Gly Gln Glu Ala Arg Pro Glu Glu  
 40 45 50  
 att ggc tgg tta aat ggc tat aat gaa acc aca ggg gaa agg ggg gac 246  
 Ile Gly Trp Leu Asn Gly Tyr Asn Glu Thr Thr Gly Glu Arg Gly Asp  
 55 60 65  
 ttt cct gga act tac gta gaa tat att gga agg aaa aaa atc tcc cct 294  
 Phe Pro Gly Thr Tyr Val Glu Tyr Ile Gly Arg Lys Lys Ile Ser Pro  
 70 75 80  
 ccc aca cca aag ccc cgg cca cct cgg cct ctt cct gtt gaa tca ggt 342  
 Pro Thr Pro Lys Pro Arg Pro Pro Arg Pro Leu Pro Val Ala Pro Gly  
 85 90 95 100  
 tct tcc aaa act gaa gca gat gtt gaa caa caa gct ttg act ctc ccc 390  
 Ser Ser Lys Thr Glu Ala Asp Val Glu Gln Gln Ala Leu Thr Ile Pro  
 105 110 115 120  
 gat ctt ccc 438

|   |     |      |
|---|-----|------|
| Asp Leu Ala Glu Glu Phe Ala Pro Pro Asp Ile Ala Pro Pro Leu Leu |     |      |
| 125   | 126 | 127  |
|   |     |      |
| tcc aag ctc gtc gaa gtc att gaa aag aac ggt ctc gaa tgg tca act |     | 461  |
| Ile Lys Leu Val Glu Ala Ile Glu Lys Lys Leu Glu Cys Ser Thr     |     |      |
| 135   | 141 | 145  |
|   |     |      |
| cta taa aca aca cag agg tcc aag aac ctc gta gaa tta cga cag ctt |     | 534  |
| Leu Tyr Arg Thr Glu Ser Ser Asn Leu Ala Glu Leu Arg Glu Leu     |     |      |
| 151   | 155 | 160  |
|   |     |      |
| ctt gat tgt gat aca ccc tcc gtc gac ttg gaa atg atc gat ctc cac |     | 582  |
| Leu Asp Cys Asp Thr Pro Ser Val Asp Leu Glu Met Ile Asp Val His |     |      |
| 165   | 170 | 175  |
|   |     |      |
| gtt ttg gct gac gct ttc aaa cgg tat ctc ctg gac tta cca aat cct |     | 630  |
| Val Leu Ala Asp Ala Phe Lys Arg Tyr Leu Leu Asp Leu Pro Asn Pro |     |      |
| 185   | 190 | 195  |
|   |     |      |
| gtc att cca gca gcc gtt tac agt gaa atg att tct tta gct cca gaa |     | 678  |
| Val Ile Pro Ala Ala Val Tyr Ser Glu Met Ile Ser Leu Ala Pro Glu |     |      |
| 200   | 205 | 210  |
|   |     |      |
| gta caa agc tcc gaa gaa tat att cag cta ttg aag aag ctt att agg |     | 726  |
| Val Gln Ser Ser Glu Glu Tyr Ile Gln Leu Leu Lys Lys Leu Ile Arg |     |      |
| 215   | 220 | 225  |
|   |     |      |
| tcg cct agc ata cct cat cag tat tgg ctt aog ctt cag tat ttg tta |     | 774  |
| Ser Pro Ser Ile Pro His Gln Tyr Trp Leu Thr Leu Gln Tyr Leu Leu |     |      |
| 230   | 235 | 240  |
|   |     |      |
| aaa cat ttc ttc aag ctc tct caa acc tcc ags aaa aat ctg ttg aat |     | 822  |
| Lys His Phe Phe Lys Leu Ser Gln Thr Ser Ser Lys Asn Leu Leu Asn |     |      |
| 245   | 250 | 255  |
|   |     |      |
| gca aga gta ctc tct gaa att ttc agc cct atg ctt ttc aga ttc tca |     | 870  |
| Ala Arg Val Leu Ser Glu Ile Phe Ser Pro Met Leu Phe Arg Phe Ser |     |      |
| 265   | 270 | 275  |
|   |     |      |
| gca gcc agc tct gat aat act gaa aac ctc ata aaa gtt ata gaa att |     | 918  |
| Ala Ala Ser Ser Asp Asn Thr Glu Asn Leu Ile Lys Val Ile Glu Ile |     |      |
| 280   | 285 | 290  |
|   |     |      |
| tta atc tca act gaa tgg aat gaa cga cag cct gca tca gca ctg cct |     | 966  |
| Leu Ile Ser Thr Glu Trp Asn Glu Arg Gln Pro Ala Pro Ala Leu Pro |     |      |
| 295   | 300 | 305  |
|   |     |      |
| cct aac cca cca aaa cct act act gta gcc aac aac ggt atg aat aac |     | 1014 |
| Pro Lys Pro Pro Lys Pro Thr Thr Val Ala Asn Asn Gly Met Asn Asn |     |      |
| 310   | 315 | 320  |
|   |     |      |
| aat atg tcc tta caa aat gct gaa tgg tac tgg gga gat atc tcg agg |     | 1062 |
| Asn Met Ser Leu Glu Asn Ala Glu Trp Tyr Trp Gly Asp Ile Ser Arg |     |      |
| 335   | 330 | 340  |
|   |     |      |
| gaa gaa gtg aat gaa aaa ctt cya gat aca gca gac ggg acc ttt ttg |     | 1110 |
| Glu Glu Val Asn Glu Lys Leu Arg Asp Thr Ala Asp Glu Thr Phe Leu |     |      |
| 345   | 350 | 355  |

|   |      |
|---|------|
| gtt cgg gat ggg tct act aaa atg cat ggt gat tat act ctt acg cta<br>Val Arg Asp Ala Ser Thr Lys Met His Gly Asp Tyr Thr Leu Thr Leu<br>361 365 371     | 1158 |
| agg aac ggg gga aat aac aaa tta atc aaa ata ttt cat cga gat ggg<br>Asn Lys Gly Asn Asn Lys Leu Lys Ile Phe His Arg Asp Gly<br>375 381 385             | 1206 |
| aaa tat ggc ttc tct gac cca tta acc ttc agt tct gtg gtt gaa tta<br>Lys Tyr Gly Phe Ser Asp Pro Leu Thr Phe Ser Ser Val Val Glu Leu<br>391 395 400     | 1254 |
| ata aac cac tac cgg aat gaa tct cta gct cag tat aat ccc aaa ttg<br>Ile Asn His Tyr Arg Asn Glu Ser Leu Ala Gln Tyr Asn Pro Lys Leu<br>405 410 415 420 | 1302 |
| gat gtc aaa tta ctt tat cca gta tcc aaa tac caa cag gat caa gtt<br>Asp Val Lys Leu Tyr Pro Val Ser Lys Tyr Glu Gln Asp Glu Val<br>425 430 435         | 1350 |
| gtc aac gaa gat aat att gaa gct gta ggg aaa aaa tta cat gaa tat<br>Val Lys Glu Asp Asn Ile Glu Ala Val Gly Lys Leu His Glu Tyr<br>440 445 450         | 1398 |
| aac act cag ttt saa gaa aaa agt cga gaa tat gat aga tta tat gaa<br>Asn Thr Gln Phe Gln Glu Lys Ser Arg Glu Tyr Asp Arg Leu Tyr Glu<br>455 460 465     | 1446 |
| gaa tat acc cgg aca tcc cag gaa atc caa atg aaa agg aca gct att<br>Glu Tyr Thr Arg Thr Ser Gln Glu Ile Gln Met Lys Arg Thr Ala Ile<br>470 475 480     | 1494 |
| gaa gca ttt aat gaa acc ata aaa ata ttt gaa gaa cag tgc cag acc<br>Glu Ala Phe Asn Glu Thr Ile Lys Ile Phe Glu Glu Gln Cys Gln Thr<br>485 490 495 500 | 1542 |
| caa gag cgg tac agt aaa gaa tac ata gaa aag ttt aaa cgt gaa ggc<br>Gln Glu Arg Tyr Ser Lys Glu Tyr Ile Glu Lys Phe Lys Arg Glu Gly<br>505 510 515     | 1590 |
| aat gag aaa gaa ata caa agg att atg cat aat tat gat aag ttg aag<br>Asn Glu Lys Glu Ile Gln Arg Ile Met His Asn Tyr Asp Lys Leu Lys<br>520 525 530     | 1638 |
| tct cga atc agt gaa att att gac agt aga aga aga ttg gaa gaa gac<br>Ser Arg Ile Ser Glu Ile Ile Asp Ser Arg Arg Arg Leu Glu Glu Asp<br>535 540 545     | 1686 |
| ttg aag aag cag gca gct gag tat cga gaa att gac aaa cgt atg aac<br>Leu Lys Lys Gln Ala Ala Glu Tyr Arg Glu Ile Asp Lys Arg Met Asn<br>550 555 560     | 1734 |
| agc att aaa cca gac ctt att cag ctg aga aag acg aga gac caa tac<br>Ser Ile Lys Pro Asp Leu Ile Gln Leu Arg Lys Thr Arg Asp Gln Tyr<br>565 570 575 580 | 1782 |
| ttg atg tgg ttg act caa aaa ggt gtt cgg caa aag aag ttg aac gag<br>Leu Met Tyr Leu Thr Gln Lys Gly Val Arg Gln Lys Lys Leu Asn Glu<br>585 591 595     | 1830 |



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12252 ECR Primer

400 2  
ggcaacttgg cagaattacg a 21

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$\alpha$ 210: 4  
 $\alpha$ 211: 3.0  
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30

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ttatgtatccc gtttttcgttgt

20

<210> 9

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atctttttttt cttttttttt

18

<210> 9

<211> 18

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18

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18

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18

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:213: Artificial Sequence

:214:

:215: Antisense Oligonucleotide

:400: 40

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18

:216: 41

:217: 18

:218: DNA

:219: Artificial Sequence

:220:

:221: Antisense Oligonucleotide

:401: 41

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18

:210: 42

:211: 18

:212: DNA

:213: Artificial Sequence

:222:

:223: Antisense Oligonucleotide

:402: 42

gacgtgttgtt tctgtctac

18

:210: 43

:211: 18

:212: DNA

:213: Artificial Sequence

:224:

<210> Antisense Oligonucleotide

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18

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18

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<212> DNA

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<4> 46

18

### STRUCTURE AND MECHANISM

— 1 —

42110 3' 7'  
42111 4' 8'  
42112 5' 9'  
42113 Argyrophilic Sequence

(223) Antisense Oligonucleotide

14000 47

14

«210» 48  
«211» 3454  
«212» DNA  
«213» *Mus musculus*

:221> CDS  
(222> 575)...(2749)

400> 48  
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agcgtgggag ctggggagctt cagagggccgc tgaagcccgag gctggggcaga ggaaggaaacg 180  
gagccggaccc ggaggtgaag ctgagagtgg agcgtggcag taaaatcaga cgcacagatgg 240  
acagtgtgac aggaacgtca gagaggattg ggcctcgctg cgcgcgttcag cttggagtca 300  
aggtgttgac aagttgttgcgaa gaaaggacacg tggggaggacg gtggcgccgc gagggagacg 360  
ctctgtttca gtcaccccccgt tgcgtggagga cagatggaca gcgcgcggac gcccagtccac 420  
ctctcttaaa cttttggata gtggccctttt gtgtctgtgt ggacacccgt tggggatttt 480  
agcccaattct ctgaactcaac ttctctttaa aacgtaaact cggacggcag tgcgtggagcc 540  
agctccctcg tggcaggggca cttagagttgc agac atg agt gca gag ggc tac cag 595

Met Ser Ala Glu Gly Tyr Gln

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taa taa gca ctg taa gac taa aap aap gaa gaa taa gag gaa gac att gag 643  
Tyr Arg Ala Leu Tyr Asp Tyr Lys Lys Glu Arg Glu Glu Asp Ile Asp

| 10   | 15  | 20  |     |
|--|-----|-----|-----|
| ttt ccc ctc ggg gac ata ctc aat gat aat ggc tcc tta ttt gtc gca 691  |     |     |     |
| Leu His Leu Cys Asp Ile Leu Thr Val Asn Lys Cys Ser Leu Val Ala      |     |     |     |
| 25   | 30  | 35  |     |
| ctt gga ttc aat gat ggc cag gaa gcc cgg ctt gaa gat att ggc tgg 739  |     |     |     |
| Leu Cys Phe Ser Asp Gly Cys Glu Ala Arg Pro Glu Asp Ile Cys Trp      |     |     |     |
| 40   | 45  | 50  | 55  |
| tta aat ggc tac aat gaa acc act ggg gag agg gga gac ttt cca gga 787  |     |     |     |
| Leu Asn Gly Tyr Asn Glu Thr Thr Gly Glu Arg Gly Asp Phe Pro Gly      |     |     |     |
| 60   | 65  | 70  |     |
| act tac gtt gaa tac att gga agg aaa aga att tca ccc cct act ccc 835  |     |     |     |
| Thr Tyr Val Glu Tyr Ile Gly Arg Lys Arg Ile Ser Pro Pro Thr Pro      |     |     |     |
| 75   | 80  | 85  |     |
| aag cct cgg ccc cct cga cgg ctt cct gtt gct cgg ggt tct tca aaa 883  |     |     |     |
| Lys Pro Arg Pro Pro Arg Pro Leu Pro Val Ala Pro Gly Ser Ser Lys      |     |     |     |
| 90   | 95  | 100 |     |
| act gaa gct gac acc gag cag caa ggg ttg ccc ctt cct gat ctg gcc 931  |     |     |     |
| Thr Glu Ala Asp Thr Glu Cys Glu Ala Leu Pro Leu Pro Asp Leu Ala      |     |     |     |
| 105  | 110 | 115 |     |
| gag cag ttt gcc cct cct gat gtt gcc cgg cct ctc ctt ata aag ctc 979  |     |     |     |
| Glu Cys Phe Ala Pro Pro Asp Val Ala Pro Pro Leu Leu Ile Lys Leu      |     |     |     |
| 120  | 125 | 130 | 135 |
| ctg gaa gcc att gag aag aaa gga ctg gaa tgt tcc act cta tac aga 1027 |     |     |     |
| Leu Glu Ala Ile Glu Lys Lys Gly Leu Glu Cys Ser Thr Leu Tyr Arg      |     |     |     |
| 140  | 145 | 150 |     |
| aca cca agc tcc agc aac cct gca gaa tta cga cag ctt ctt gat tgt 1075 |     |     |     |
| Thr Gln Ser Ser Asn Pro Ala Glu Leu Arg Gln Leu Leu Asp Cys          |     |     |     |
| 155  | 160 | 165 |     |
| gat gcc gcg tca ttt gac ttt ggg atg atc gac gta ccc gtc tta gca 1123 |     |     |     |

|   |     |     |     |
|---|-----|-----|-----|
| Asp Ala Ala Ser Val Asp Leu Glu Met Ile Asp Val His Val Leu Ala       |     |     |     |
| 170   | 175 | 180 |     |
| gat gct ttc aaa cgc tat ctc gcc gac tta cca aat cct gtc att cct 1171  |     |     |     |
| Asp Ala Phe Lys Arg Tyr Leu Ala Asp Leu Pro Asn Pro Val Ile Pro       |     |     |     |
| 185   | 190 | 195 |     |
| gta gct gtt tac aat gag atg atg tct tta gcc caa gaa cta gag agc 1219  |     |     |     |
| Val Ala Val Tyr Asn Glu Met Met Ser Leu Ala Glu Leu Glu Ser           |     |     |     |
| 200   | 205 | 210 | 215 |
| cct gaa gac tgc atc gag ctg ttg aag aag ctc att aga ttg cct aat 1267  |     |     |     |
| Pro Glu Asp Cys Ile Gln Leu Leu Lys Leu Ile Arg Leu Pro Asn           |     |     |     |
| 220   | 225 | 230 |     |
| ata cct cat cag tgt tgg ctt acg ctt cag tat ttg ctc aag cat ttt 1315  |     |     |     |
| Ile Pro His Gln Cys Trp Leu Thr Leu Gln Tyr Leu Leu Lys His Phe       |     |     |     |
| 235   | 240 | 245 |     |
| ttc aag ctc tct caa gcc tcc agc aaa aac ctt ttg aat gca aga gtc 1363  |     |     |     |
| Phe Lys Leu Ser Gln Ala Ser Ser Lys Asn Leu Leu Asn Ala Arg Val       |     |     |     |
| 250   | 255 | 260 |     |
| ctc tct gag att ttc agc ccc gtg ctt ttc aga ttt cca gcc gct agc 1411  |     |     |     |
| Leu Ser Glu Ile Phe Ser Pro Val Leu Phe Arg Phe Pro Ala Ala Ser       |     |     |     |
| 265   | 270 | 275 |     |
| tct gat aat act gaa cac ctc ata aaa gcg ata gag att tta atc tca 1459  |     |     |     |
| Ser Asp Asn Thr Glu His Leu Ile Lys Ala Ile Glu Ile Leu Ile Ser       |     |     |     |
| 280   | 285 | 290 | 295 |
| acg gaa tgg aat gag aga cag cca gca cca gca ctg cct ccc aaaa cca 1507 |     |     |     |
| Thr Glu Trp Asn Glu Arg Gln Pro Ala Pro Ala Pro Pro Lys Pro           |     |     |     |
| 300   | 305 | 310 |     |
| ccc aag ccc act act gta gcc aac aac agc atg aac aac aat atg tcc 1555  |     |     |     |
| Pro Lys Pro Thr Thr Val Ala Asn Asn Ser Met Asn Asn Asn Met Ser       |     |     |     |
| 315   | 320 | 325 |     |

|   |      |     |     |
|---|------|-----|-----|
| ttg cag gat gct gaa tgg tac tgg gga gac atc tca aac gaa gaa gtc | 1603 |     |     |
| Leu Gln Asp Ala Glu Trp Tyr Trp Gly Asp Ile Ser Arg Glu Glu Val |      |     |     |
| 330   | 335  | 340 |     |
| aat gaa aaa ctc cga gac act gct gat gaa acc ttt ttg gta cga gac | 1651 |     |     |
| Asn Glu Lys Leu Arg Asp Thr Ala Asp Gly Thr Phe Leu Val Arg Asp |      |     |     |
| 345   | 350  | 355 |     |
| gca tct act aaa atg cac ggc gat tac act ctt aca cct agg aaa gga | 1699 |     |     |
| Ala Ser Thr Lys Met His Gly Asp Tyr Thr Leu Thr Pro Arg Lys Gly |      |     |     |
| 360   | 365  | 370 | 375 |
| gga aat aac aaa tta atc aaa atc ttt cac cgt gat gga aaa tat ggc | 1747 |     |     |
| Gly Asn Asn Lys Leu Ile Lys Ile Phe His Arg Asp Gly Lys Tyr Gly |      |     |     |
| 380   | 385  | 390 |     |
| ttc tct gat cca tta acc ttc aac tct gtc gtt gag tta ata aac cac | 1795 |     |     |
| Phe Ser Asp Pro Leu Thr Phe Asn Ser Val Val Glu Leu Ile Asn His |      |     |     |
| 395   | 400  | 405 |     |
| taa cgg aat gag tct tta gct cag tac aac ccc aag ctg gat gtc aag | 1843 |     |     |
| Tyr Arg Asn Glu Ser Leu Ala Gln Tyr Asn Pro Lys Leu Asp Val Lys |      |     |     |
| 410   | 415  | 420 |     |
| ttg ctc tac cca gtc tcc aaa tac cag cag gat caa gtt gtc aaa gaa | 1891 |     |     |
| Leu Leu Tyr Pro Val Ser Lys Tyr Gln Gln Asp Gln Val Val Lys Glu |      |     |     |
| 425   | 430  | 435 |     |
| gat aat att gaa gtc gta ggg aaa aaa tta cat gaa tat aat act caa | 1939 |     |     |
| Asp Asn Ile Glu Ala Val Gly Lys Leu His Glu Tyr Asn Thr Gln     |      |     |     |
| 440   | 445  | 450 | 455 |
| ttt caa gaa aaa aat cgg gaa tat gat aga tta tat gag gag tac acc | 1987 |     |     |
| Phe Gln Glu Lys Ser Arg Glu Tyr Asp Arg Leu Tyr Glu Glu Tyr Thr |      |     |     |
| 460   | 465  | 470 |     |
| cgt act tcc tag gaa atc caa atg aaa aca acg gct atc gaa gca ttt | 2035 |     |     |
| Arg Thr Ser Gln Glu Ile Gln Met Lys Arg Thr Ala Ile Glu Ala Phe |      |     |     |
| 475   | 480  | 485 |     |



635

640

645

gtc cgg gag agc agt aag cag ggc tgc tat gct tgc tcc gta gtc gta 1563  
 Val Arg Glu Ser Ser Lys Gln Gly Cys Tyr Ala Cys Ser Val Val Val  
 650 655 660

gac ggc gaa gtc aag cat tgc gtc att aac aag act gct acc ggc tat 1611  
 Asp Gly Glu Val Lys His Cys Val Ile Asn Lys Thr Ala Thr Gly Tyr  
 665 670 675

ggc ttt gcc gag ccc tac aac ctg tac agc tcc ctg aag gag ctg gtg 2659  
 Gly Phe Ala Glu Pro Tyr Asn Leu Tyr Ser Ser Leu Lys Glu Leu Val  
 680 685 690 695

cta cat tatcaa cac acc tcc ctc gtg cag cac aat gac tcc ctc aat 1707  
 Leu His Tyr Gln His Thr Ser Leu Val Gln His Asn Asp Ser Leu Asn  
 700 705 710

gtc aca cta gca tac cca gta tat gca caa cag agg cga tga 2749  
 Val Thr Leu Ala Tyr Pro Val Tyr Ala Gln Gln Arg Arg \*  
 715 720

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<212> DNA

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20

<210> 70

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

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<400> 70

30

## INTRODUCTION

J. POLYMER SCI.: PART A

21106 14

### 4212A-DNA

### 4.2.1.3. Artificial Sequence

<200>

### 4.223: Antisense Oligonucleotide

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(210) 72

<211> 20

<212> DNA

### 4.113. Artificial Sequence

4220

## 4223: Antisense Oligonucleotide

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20

(210) 73

4.2.1.2. 20

<212> DNA

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• 220 •

<223> Antisense Oligonucleotide

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